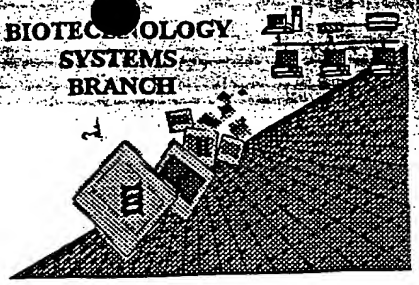
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/836,911

Source: OIPE

Date Processed by STIC: 5/3/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001
TIME: 15:56:14

Input Set : A:\402iseq.001
Output Set: N:\CRF3\05032001\I836911.raw

PS

SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Hadlaczky, Gyula
7 Szalay, Aladar
C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
12 (iii) NUMBER OF SEQUENCES: 34
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
16 (B) STREET: 4350 La Jolla Village Drive, 6th Floor
17 (C) CITY: San Diego
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 92122
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ Version 1.5
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/836,911
C--> 30 (B) FILING DATE: 17-Apr-2001
50 (C) CLASSIFICATION:
C--> 47 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/835,682
34 (B) FILING DATE: 10-APR-1997
38 (A) APPLICATION NUMBER: 08/695,191
39 (B) FILING DATE: 07-AUG-1996
43 (A) APPLICATION NUMBER: 08/682,080
44 (B) FILING DATE: 15-JUL-1996
48 (A) APPLICATION NUMBER: 08/629,822
49 (B) FILING DATE: 10-APR-1996
52 (viii) ATTORNEY/AGENT INFORMATION:
53 (A) NAME: Seidman, Stephanie L
54 (B) REGISTRATION NUMBER: 33,779
55 (C) REFERENCE/DOCKET NUMBER: 24601-402I
58 (ix) TELECOMMUNICATION INFORMATION:
59 (A) TELEPHONE: 858-450-8403
60 (B) TELEFAX: 858-587-5360
61 (C) TELEX:
63 (2) INFORMATION FOR SEQ ID NO: 1:
65 (i) SEQUENCE CHARACTERISTICS:
66 (A) LENGTH: 1293 base pairs
67 (B) TYPE: nucleic acid
68 (C) STRANDEDNESS: single
69 (D) TOPOLOGY: linear
71 (ii) MOLECULE TYPE: Genomic DNA

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(iii) HYPOTHETICAL: NO
C--> (iv) ANTI-SENSE: NO
W--> (v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT 60
TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT 120
TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN 180
GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTC AGTTTTCCTC 240
GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNCC GTGATTTTCA GTTTTCTCGC 300
CAGATTCCAG GTCCTATAAT GTGCATTTCT CATTTNNCAC GTTTTTCAGT GATTTCGTCA 360
TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT 420
ATTCCATGTC CTACAATGAT CATTTTTAAT TTTCCACCTT TTCATTTTTC CACGCCATAT 480
TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTTCT CGCCATATTC 540
CAGGTCCTAC AGTGTGCATT CCTCATTTTT CACCTTTTTC ACTGATTTCG TCATTTTTCA 600
AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTCAG TTATCTTGTC ATATTCCATG 660
TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTTGACG 720
TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC 780
CTAATAGTGT GCATTTCTCA TTTTTCACGT TTTTCAGTGA TTTCGTCATT TTTTCCAGTT 840
GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTTT CTTGCTATAT TCCATGTCCT 900
ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTTC TCACCATATT TCACGTCCTA 960
AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCCTT GCCATATTCC AGGTCCTACA 1020
GTGTGCATTT CTCATTTTTC ACGTTTTTCA GTAATTTCTT CATTTTTTAA GCCCTCAAAT 1080
GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG 1140
ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTCATCGGC ACATTTCACG TCCTAAAGTG 1200
TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG 1260
CATTTCTCAT TTTTCACGTT TTTCAGTGAA TTC 1293

(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1044 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
C--> (iv) ANTI-SENSE: NO
W--> (v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AGGCCTATGG TGAAAAAGGA AATATCTTCC CCTGAAAACT AGACAGAAGG ATTCTCAGAA 60
TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTTCTTTT GATAGAGCAG 120
TTTTGAAACA CTCTTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC 180
CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT 240
TGGGATGTTT CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA 300
ACACTCTTTT TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA CTGCGGTGAA 360
AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT 420
GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT 480

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Input Set : A:\402iseq.001
Output Set: N:\CRF3\05032001\I836911.raw

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 128  TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCGTTGG GAAACGGGAT     540
 129  TACATATAAA AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG     600
 130  TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT     660
 131  GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA     720
 132  AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT     780
 133  GAAGCTTTCT TTTGATAGAG GCAGTTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT     840
 134  ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG     900
 135  CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT     960
 136  CAGAGAGCAG GTTTGAACAC TCTTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT    1020
 137  CAGGGGGGAT CCTCTAGAAT TCCT                                          1044
 141 (2) INFORMATION FOR SEQ ID NO: 3:
 143      (i) SEQUENCE CHARACTERISTICS:
 144           (A) LENGTH: 2492 base pairs
 145           (B) TYPE: nucleic acid
 146           (C) STRANDEDNESS: single
 147           (D) TOPOLOGY: linear
 149     (ii) MOLECULE TYPE: Genomic DNA
 150    (iii) HYPOTHETICAL: NO
C--> 151     (iv) ANTI-SENSE: NO
W--> 152      (v) FRAGMENT TYPE:
 153     (vi) ORIGINAL SOURCE:
 154     (ix) FEATURE:
 156     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 158  CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCCTTACT ACTCAGATGG GGTGGCCGAG      60
 159  TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT     120
 160  GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA     180
 161  GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG     240
 162  AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT     300
 163  TGCTATCCTG GGGTTCAACC CCCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT     360
 164  ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG     420
 165  AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA     480
 166  AGGGCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT     540
 167  TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA     600
 168  TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA     660
 169  CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG     720
 170  GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG     780
 171  TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA     840
 172  GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA     900
 173  AGAGTTCTTG TTTTTCCTTC AGCAATTTGT CATTTTTAAA AGAGTTTAGC AATTCTAACA     960
 174  GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA    1020
 175  ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG    1080
 176  CATTTCTTGN NTTTNGGCTG TTTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT    1140
 177  GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTC TTCAATATGA GGCTTGCTTT    1200
 178  TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC    1260
 179  TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAAATTC ATTACCAAAC CCAAAGGCAG    1320
 180  ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG    1380
 181  GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTTT CGTCTATATC CATATCATTT    1440
 182  CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTTGGG AAAGACACAG GATAGTGGGC    1500
 183  TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA    1560
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Input Set : A:\402iseq.001
Output Set: N:\CRF3\05032001\I836911.raw

GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG 1620
CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA 1680
GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAATGTCA 1740
GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA 1860
ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC 1920
GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG 2100
GCTGTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT 2220
TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG 2400
CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG 2460
ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

C--> (iv) ANTI-SENSE: NO

W--> (v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGGAATTCA TTGGGATGTT TCAGTTGA 28

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

C--> (iv) ANTI-SENSE: NO

W--> (v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/836,911

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TIME: 15:56:14

Input Set : A:\402iseq.001
Output Set: N:\CRF3\05032001\I836911.raw

```
     245           (D) TOPOLOGY: linear
W--> 247      (ii) MOLECULE TYPE: DNA
     248     (iii) HYPOTHETICAL: NO
C--> 249      (iv) ANTI-SENSE: NO
W--> 250       (v) FRAGMENT TYPE:
     251      (vi) ORIGINAL SOURCE:
     252     (ix) FEATURE:
     254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
     256 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC                47
     260 (2) INFORMATION FOR SEQ ID NO: 7:
     262       (i) SEQUENCE CHARACTERISTICS:
     263            (A) LENGTH: 25 base pairs
     264            (B) TYPE: nucleic acid
     265            (C) STRANDEDNESS: single
     266            (D) TOPOLOGY: linear
     268      (ii) MOLECULE TYPE: Genomic DNA
     269     (iii) HYPOTHETICAL: NO
C--> 270      (iv) ANTI-SENSE: NO
W--> 271       (v) FRAGMENT TYPE:
     272      (vi) ORIGINAL SOURCE:
     273     (ix) FEATURE:
     275      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
     277 CGATTTAAAT TAATTAAGCC CGGGC                                       25
     280 (2) INFORMATION FOR SEQ ID NO: 8:
     282       (i) SEQUENCE CHARACTERISTICS:
     283            (A) LENGTH: 27 base pairs
     284            (B) TYPE: nucleic acid
     285            (C) STRANDEDNESS: single
     286            (D) TOPOLOGY: linear
     288      (ii) MOLECULE TYPE: Genomic DNA
     289     (iii) HYPOTHETICAL: NO
C--> 290      (iv) ANTI-SENSE: NO
W--> 291       (v) FRAGMENT TYPE:
     292      (vi) ORIGINAL SOURCE:
     293     (ix) FEATURE:
     295      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
     297 TAAATTTAAT TAATTCGGGC CCGTCGA                                     27
     299 (2) INFORMATION FOR SEQ ID NO: 9:
     301       (i) SEQUENCE CHARACTERISTICS:
     302            (A) LENGTH: 69 base pairs
     303            (B) TYPE: nucleic acid
     304            (C) STRANDEDNESS: single
     305            (D) TOPOLOGY: linear
     307      (ii) MOLECULE TYPE: Genomic DNA
     310     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
     312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT    48
     313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
W--> 315 GTC ACA AAC AGT GCA CCT ACT                                     69
     316 Val Thr Asn Ser Ala Pro Thr
```

(Per Sequence Rules, Number the amino acids under every 5 amino acids — do not use TAB codes between numbers 5/3/01

Please edit all subsequent sequences containing these errors

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001
TIME: 15:56:15

Input Set : A:\402iseq.001
Output Set: N:\CRF3\05032001\I836911.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2
L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3
L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4
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L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5
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L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6
L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
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L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8
L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:339 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]
L:433 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:438 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11
L:434 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11
L:452 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:453 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12
L:471 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:472 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13
L:512 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14
L:553 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:554 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15

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Input Set : A:\402iseq.001
Output Set: N:\CRF3\05032001\I836911.raw

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L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
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L:1735 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:1764 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1765 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20
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L:1790 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:1813 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1814 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:1837 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1838 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:1866 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1867 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24
L:1896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1897 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:1914 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1915 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:1932 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1933 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:1950 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1951 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28
L:1968 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1969 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:1987 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1988 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:2005 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2006 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31
L:2023 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2024 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:2041 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2042 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:2059 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2060 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34